

## CLAIMS

We claim:

1. A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:
  - 5 (A) receiving a protein backbone structure with variable residue positions;
  - (B) establishing a group of potential rotamers for each of said variable residue positions, wherein at least one variable residue position has rotamers from at least two different amino acid side chains; and
  - 10 (C) analyzing the interaction of each of said rotamers with all or part of the remainder of said protein backbone structure to generate a set of optimized protein sequences, wherein said analyzing step includes a Dead-End Elimination (DEE) computation.
2. A method executed by a computer under the control of a program, said computer including a memory for storing said program, said method comprising the steps of:
  - 15 (A) receiving a protein backbone structure with variable residue positions;
  - (B) classifying each variable residue position as either a core, surface or boundary residue;
  - (C) establishing a group of potential rotamers for each of said variable residue positions, wherein at least one variable residue position has rotamers from at least two different amino acid side chains; and
  - 20 (D) analyzing the interaction of each of said rotamers with all or part of the remainder of said protein to generate a set of optimized protein sequences.
3. A method according to claim 2 wherein said analyzing step comprises a DEE computation.
4. A method according to claim 1 or 2 wherein said set of optimized protein sequences comprises the globally optimal protein sequence.
5. A method according to claim 1 or 3 wherein said DEE computation is selected from the group  
25 consisting of original DEE and Goldstein DEE.
6. A method according to claim 1 or 2 wherein said analyzing step includes the use of at least one scoring function.
7. A method according to claim 6 wherein said scoring function is selected from the group consisting of a Van der Waals potential scoring function, a hydrogen bond potential scoring  
30 function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

8. A method according to claim 6 wherein said analyzing step includes the use of at least two scoring functions.
9. A method according to claim 6 wherein said analyzing step includes the use of at least three scoring functions.
- 5 10. A method according to claim 6 wherein said analyzing step includes the use of at least four scoring functions.
11. A method according to claim 1 or 2 further comprising testing at least one member of said set to produce experimental results.
12. A method according to claim 4 further comprising
- 10 (D) generating a rank ordered list of additional optimal sequences from said globally optimal protein sequence.
13. A method according to claim 12 wherein said generating includes the use of a Monte Carlo search.
14. A method according to claim 2 wherein said analyzing step comprises a Monte Carlo
- 15 computation.
15. A method according to claim 12 further comprising:
- (E) testing some or all of said protein sequences from said ordered list to produce potential energy test results.
16. A method according to claim 15 further comprising:
- 20 (F) analyzing the correspondence between said potential energy test results and theoretical potential energy data.
17. An optimized protein sequence generated by the method of claim 1 or 2.
18. A nucleic acid sequence encoding a protein sequence according to claim 17.
19. An expression vector comprising the nucleic acid of claim 18.
- 25 20. A host cell comprising the nucleic acid of claim 18.

21. A protein having a sequence that is at least about 5% different from a known protein sequence and is at least 20% more stable than the known protein sequence.

22. A computer readable memory to direct a computer to function in a specified manner, comprising:

- 5        a side chain module to correlate a group of potential rotamers for residue positions of a protein backbone model;
- a ranking module to analyze the interaction of each of said rotamers with all or part of the remainder of said protein to generate a set of optimized protein sequences.

10       23. A computer readable memory according to claim 22 wherein said ranking module includes a van der Waals scoring function component.

24. A computer readable memory according to claim 22 wherein said ranking module includes an atomic solvation scoring function component.

25. A computer readable memory according to claim 22 wherein said ranking module includes a hydrogen bond scoring function component.

15       26. A computer readable memory according to claim 22 wherein said ranking module includes a secondary structure scoring function component.

27. A computer readable memory according to claim 22 further comprising  
         an assessment module to assess the correspondence between potential energy test results and theoretical potential energy data.